

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 16, 2003, 15:50:54 ; Search time 2481.53 seconds
(without alignments)
16465.78 Million cell updates/sec

Title: US-09-497-967-3

Perfect score: 1404

Sequence: 1 atgaaataataatttagt.....tgattcttattattatta 1404

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sv:*
13: gb_un:*
14: gb_vt:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sv:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1404	100.0	3026	3	AF324424 Ichthyoph
2	254.4	18.1	1520	3	AF405431 Ichthyoph
3	252.6	18.0	2486	3	AF140273 Ichthyoph
4	214.6	15.3	1249	3	ICVIMANT M92907 Ichthyophth
5	96	6.8	175748	2	AC120669 Rattus no
6	96	6.8	180903	2	AC120669 Rattus no
7	95.2	6.8	186935	2	AC120669 Rattus no
8	92.4	6.6	179553	2	AC022322 Homo sapi
9	90.8	6.5	131274	2	AC022322 Homo sapi
10	90.8	6.5	176822	2	AC096869 Rattus no
11	85.6	6.1	261604	2	AC099174 Rattus no
12	85.4	6.1	127354	2	AC119819 Mus muscu
13	85.4	6.1	155019	2	AC117014 Rattus no
14	81	5.8	35793	5	AY016024 Takifugu
15	81	5.8	84472	2	AC096684 Takifugu
16	80.2	5.7	132449	9	AL365272 Human DNA
17	77.2	5.5	22398	5	FRU271723 Fugu rubr
18	77	5.5	85786	9	AL162582 Human DNA
19	76.6	5.5	10115	5	AF397467 Ictalurus
20	75.8	5.4	183413	2	AC131200 Rattus no
21	75.6	5.4	170985	2	AC096032 Rattus no
22	74.6	5.3	204259	2	AC110817 Mus muscu
23	74	5.3	172307	2	AC044842 Homo sapi
24	72.4	5.2	189461	2	AC119627 Rattus no
25	72.4	5.2	191841	2	AC121374 Rattus no
26	72	5.1	134558	2	AC125757 Rattus no
27	72	5.1	180668	2	AC020857 Mus muscu
28	69.8	5.0	666	8	AF41305052 Zea mays
29	69.2	4.9	172853	9	AC084361 Homo sapi
30	68.2	4.9	71553	2	AC096997 Takifugu
31	68	4.8	154141	2	AC121042 Rattus no
32	68	4.8	162269	9	AC000097 Homo sapi
33	67.8	4.8	184830	2	AC113220 Rattus no
34	67.2	4.8	185994	2	AC002042 Homo sapi
35	67.2	4.8	300994	2	AC129317 Mus muscu
36	66.2	4.7	131346	2	AC119558 Rattus no
37	66	4.7	158615	2	AC117835 Rattus no
38	65.8	4.7	101534	2	AC108576 Rattus no
39	65.8	4.7	298283	3	AF003782 Drosophil
40	64.8	4.6	177035	2	AC099443 Rattus no
41	64.4	4.6	186558	2	AC079031 Homo sapi
42	64.4	4.6	325808	2	AC121787 Mus muscu
43	64.2	4.6	187617	2	AC118993 Rattus no
44	64	4.6	100726	2	AC116961 Dictyoste
45	63.8	4.5	177435	2	AC128321 Rattus no

ALIGNMENTS

RESULT 1
AF324424
LOCUS
DEFINITION
Ichthyophthirius multifiliis immobilization antigen isoform
ACCESSION
AF324424
VERSION
AF324424.1
KEYWORDS
GI:12698726
SOURCE
ichthyophthirius multifiliis.
ORGANISM
Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE
1 (bases 1 to 3026)
AUTHORS
Lin, Y., Lin, T.L., Wang, C.C., Wang, X., Stieger, K., Klopfeisch, R.
and Clark, T.G.

AF324424 3026 bp DNA linear INV 27-FEB-2002
Ichthyophthirius multifiliis immobilization antigen isoform
(TAG52A) gene, complete cds.

DEFINITION Ichthyophthirius multifiliis 52kDa immobilization antigen variant B
protein mRNA, complete cds.
ACCESSION AF405431
VERSION AF405431.1 GI:15290741
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
Source
CDS
BASE COUNT 493 a 255 c 256 g 516 t
ORIGIN
Query Match 18.18; Score 254.4; DB 3; Length 1520;
Best Local Similarity 55.18; Pred. No. 3e-35;
Matches 794; Conservative 0; Mismatches 546; Indels 102; Gaps 11;
QY 1 ATGAAAAATAATATTAGTAATAATTGATTATTTTCATTATTTATCAATTAATAATTAATCT 60
DB 41 ATGAAATTAATATTTTAAATAATTTTCGTTATTTTCCTTATTTATTAATGAATTAAGAGCT 100
QY 61 GCTAATTCCTGTTGGAAGTAACTAACACAGCCGGATAAGTTGATGATCTAGGAAT 120
DB 101 GTTAATTGCTTAATGGTGGTGCATATTCGGAATGGATAATCTGATACAGGAGCTGCAGAT 160
QY 121 CCTGCAAAATGCTTAATTTGTAGAAAACTTTTATTAATAATAATGCTGCTGCT----- 174
DB 161 ATAAATCTGTACTCATCTGCTAAAAACACTTTTACTTTTAAATGGTGAATCTGCTGAGGT 220
QY 175 -----TTGGTTCTGGTGGTACGTACGTACAGTGTACACCTGTGTCATAA 213
DB 221 CAGGCTCCTGGTGTGTACAAATTCACAGGTGTTAGTCAGTGCATAGCTTGCCAAAGTA 280
QY 214 AAAAAAGATGCTGCTTAACCAATCCACCTGCTACTGCTTAATTTAGTCACATAATGT 273
DB 281 CACAAA---GCCGATTCACACAGATAAGGTGGTGGTATGCTAAATTTAGCCCGCATAAATGT 337
QY 274 AACGTTAAATGCCCTGCTGTTACCGCAATTTGCAGGTGGAGCAACAGATTATCCAGCAATA 333

DB 338 AGCAACTATATGTCCTGCTGCACCTGCAGTTGAAGATGGATCACCTACTTTTACTTAATCC 397
QY 334 ATCACAGAAATGTTAATTTAGTAGAATTAATTTTATAAATAAATGCTCCAAATTTTAAAT 393
DB 398 CTCACATAATGTTAATTTGAACCACTAACTTTTACTTTAATGGTGGTAATCCTACAGGT 457
QY 394 GCAGGTGCTAGTACATGCACAGCTTCTGCGGTAAACAGAGTTGGTGGTGCATGACTGCT 453
DB 458 CAGGCTCCGTGGTCTGGATAATTCGATCCCACTTAATGATGCAAAATCCCTGATCTGCT 517
QY 454 GGTAAATGCCGTACCATAGTCGCATAATGTAAGTGGCATGCTCTACTGCTACTGCATCT 513
DB 518 AATAATCC-----TGAAGTTCCCTAATGTTCTAGCCCTAATGGTTAATGCGCTA 565
QY 514 GATGATGGAGTAACTACTGATTATGTTAGATCATTTACAGAAATGTTTAAATGTAGACTT 573
DB 566 GCTTGGCTAAGTAACA---AGTCTGATTCTCAATTAAGACCAAGGTGCTTAGGCTAATTTA 622
QY 574 AACTTTTACTAATAGTGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 633
DB 623 GCCACATAATGTAACAATGAATGCTCTACTGGCACTGCTATTCAGACGGAGCAATATTT 682
QY 634 ACACCTTGTCCGGCAATTAACCTGCTAATGTTGCTTAAGCTACTTTAGGTAATGATGCT 693
DB 683 ATTTATACTTAATCAATCTCATAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 742
QY 694 ACAATAACCGCATATGTAACGTTGCATGCCCTGATGCTACTATAGTGGTGGAGTA 753
DB 743 -----GGCAATCCCTCAGCTCAGAAATCCCTGGTAATGGA 775
QY 754 AATAATGGGTAGCACAAAACACTGAATGTACTAATTTGCTGCTCACTTTTACAATAAT 813
DB 776 TAATTCACCTCCAGGTTAATGATTGCAAAATCCTGATGCTGCTACTGCTGCTTAATTCCT 835
QY 814 AATGCTCCTAATTTCAATCCAGGTAATGATACATGCTGCTACTGCTGCTGCTGCTGCTGCT 873
DB 836 ATGGTTCC-----TGGCCCTAATAGTAATAGTAAATGCGTGTGCTGCGAATCAAAAAGACC 886
QY 874 TATGTTGCTGAAGCAGCTGCGAGTGGTGGCTGCTACTTTAGCCAAATAATGTAATATTTGCA 933
DB 887 AA---TTCTTAATCAGATCAGGCTTTGAGGCTAATTTAGCCGCTAATGTTGGCACTGAA 943
QY 934 TCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 990
DB 944 TGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1003
QY 991 GAATGCTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1050
DB 1004 TAATGCTGTTAATTTGTAAGCTGGCTTTTACT---AAATAGTAAATTTTCGAAGCAGGTAAA 1060
QY 1051 AGTAGATGCAAAAGCATGTCAGCAAAATAAGTTTAAAGCGCTGTAGCAACTGCGAGGTGGT 1110
DB 1061 AGTTAATGCAATAAGTGTGCAAGTAAATAAAT---GTTTCAGCACTGCTGCTCCAGGTAAAT 1117
QY 1111 ACTGCTACTTTAATTTGCTAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1170
DB 1118 AGTCTACTTCCAGCCACATATGTTTAAACAGATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1177
QY 1171 GGAACAACATCTACTTATAAATAAGCAGCATCTGAATGCTGTTAAATGCTGCTGCCAATTT 1230
DB 1178 GGTACATCACTAATTTTGTAGCTTTTAGCAAGTGAATGTACTAAATGTTAGGCTAACITTT 1237
QY 1231 TATACTACAAAATAAATGATGGGTAGCAGGTATTTGATACATGTAATGTAATGTAATGTAATGTA 1290
DB 1238 TATGATCAAAAACATCTGCTTTTGGCAGCAGGTACTGATACATGTAATGTAATGTAATGTAATGTA 1297
QY 1291 AAATTAATCTTCTGCGCTGAAGCTAATTTACCTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1350
DB 1298 AAATTAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1357
QY 1351 G-----ATTTCGCTAATTTTATCAATTTTCTTATTTATTTATTTATTTATTTATTTATTTA 1401

Thu Feb 20 11:10:09 2003

us-09-497-967-3.rge

Db	1358	GCAGTTCACCTTCGCAAAATTTTATCATGTCTTAATATTATTCTTCTATTG	1417
QY	1402	TT 1403	
Db	1418	TT 1419	
RESULT 3			
AF140273			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
AF140273.1	GI:4868370		
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
gene			
mRNA			
CDS			
sig_peptide			
mat_peptide			
BASE COUNT			
ORIGIN			
Query Match			

Best Local Similarity	56.7%	Pred. No. 5.6e-35;	
Matches	660;	Conservative	0; Mismatches 394; Indels 111; Gaps 6;
QY	344	GTGTTAATTTGTAAGTAATTAATTTTATATAATGAAATGCTCCAAATTTTAAATGCGAGGTGCTA	403
Db	599	GTGCTGCTTAAAGGAGAAGCTAATGGTAATTAACCTTTTCGAGCAAAATATGCTGCTAGAG	658
QY	404	GTACATGCACAGCTTGTCCGGTAACAGAGTTGGTGGTGAATGACTGCTGGTAATGCGC	463
Db	659	GTATATGTGTACCATGCGCAAAATAACAGAGTAGGCTCTGTACCAATGCGAGGTGACTTAG	718
QY	464	CTACCATAGTCGCATAATGTAACGTCGCATGCTACTGTTGCTGCTGCTGCTGCTGCTGCTG	523
Db	719	CTACTTTAGCCACATAAATGTCAGTACTTAATGTCTCTACTGCGCAGTCTGCTGCTGCTG	778
QY	524	TAACTACTGATTATGTTAGATCATTCACAGAAATGTTAAATGATGACTTAACTTAACTTTACT	583
Db	779	TGACAGATGTTTTGATAGATCAGCGCATATGTTGTTAAATGCAACCTAACTTTTACT	838
QY	584	ATAATGGTAATTAATGGTAATGTAATCTCTTTCAATCCAGGTAAAGTTAATGCACACCTTGT	643
Db	839	ATAATGGTGGTCTCTTAAGGTGAAGCTCTGCGCTTTAAAGTTTTCGCTGCTGCTGCTG	898
QY	644	CGCAATTAACCTGCT-----AATG	664
Db	899	CGCTGCGAGGTGTTGCTGCCGTTACTAGTTAATGTTGCTGCTGCTGCTGCTGCTGCTGCTG	958
QY	665	TTGCTTAACTACTTTTAGTAAATGATGTACAAATAACCGCATATGTAACCTTGCATGCC	724
Db	959	ATTCCTCTCCACTGCAGTGCCTAAGCTAATTTAGCCACATAATGTAGCAATTAATGTC	1018
QY	725	CTGATGGTACTATAGTGTCTGCTGGAGT---AAATAATGGGTAGCACAAACCACTGAAT	781
Db	1019	CTACTGCCACTGTACTGTATGATGAGTGACACTTGTGTTTTTAATACATCAGCCACTAT	1078
QY	782	GTACTAATGTTGCTCTCTAACTTTTACAAATAATGCTCTCTAACT-----	826
Db	1079	GTGTTAAATGCAGACCTACTTTTACTATAATGGTGGTCTCTCTTAAGGTGAAGCTCCTG	1138
QY	827	-----TCAATCCAGGTAAATGATCAT	847
Db	1139	CGCTTAAAGTTTGTGCTGCTGCCGCTGCGAGGTGTTGCTGCCGTTACTAGTTAAT	1198
QY	848	GCTACTCTGCCAGCAAAATAAAGATTATGGTCTGAAGCCACTGCAGTGGTGGCGCTA	907
Db	1199	GTGTACCTTGCCAAATAACAAACAGATTCCT---GCCACTGCAGTGCCTAAGCTA	1255
QY	908	CTTTAGCCAAATAATGTAATTTGTCATGCCCTGATGGTACTGCAATGCTAGTGGCA	967
Db	1256	ATTTAGCCACATAATGTCAGTACTTAATGTCCAACCTGCCACTGCAATTCAGACGGAGTGA	1315
QY	968	CTAATTATGTAATTTATTAACAGAAATGCTAAATGTCGCTAACTTTTATTTTATG	1027
Db	1316	CACITGTTTTTAGTAATTCATCCACATAATGTTCTTAATGCAATGCTAATTTTATTTA	1375
QY	1028	GTAATAATTTCTAGGAGGAAGTAGTAGTGAAGCATGTCCAGCAATAAAGTTTAA	1087
Db	1376	ATGTTAATTTGCAAGCAGGTAAAGTTAATGTTTAAAGTGTCCAGTAAGTAAACT---A	1432
QY	1088	GCCTGTAGCAACTGCGAGGTGGTACTGCTACTTTTAAATGCAATGTCCTTGAATGCC	1147
Db	1433	CTCCAGCACATGCTCCAGGTAAATGCTACTTAAAGCCACATAATGTTTGAACCATGTC	1492
QY	1148	CTGCTGTACTGTACTCACCAGTGAACACATCTACTTATAAATAAGCAGCATCTGAAT	1207
Db	1493	CTGCTGTACTGTACTGTATGATGGAACATCACTAATTTTGTAGCTTCGCAACTGAAT	1552
QY	1208	GTGTTAAATGTCGCCAACTTTTATATACTACAAATAAATGATTTGGTAGCAGGTATTG	1267
Db	1553	GTACTAATGTTCTGCTGGCTTTTTCATCAAAACAACTGGTTTACAGCAGGTACTG	1612
QY	1268	ATACATGTACTAGTTGTAATAAATAAATAAATTAATCTGCGCTGAAGCTTAATTTACCTGAAT	1327

946	CTCCAGCACATGCTCCAGTAATACTGCTACTTAAAGCCACATAATGTTTGACCACATGTC	1005
1148	CTGCTGGTACTGACTACCCGATGGACACACATCTACTTATAATAAGCAGCATCTGAAT	1207
1006	CTGCTGGTACAGTACTGTGATGATGGAACATCAACTAATTTTGTAGTTCGCGCAACTGAAT	1065
1208	GTGTTAAATGTGCTGCCAACTTTTATCTACTACAAATAAATGATGGTGGTAGCAGGTATG	1267
1066	GTACTAAATGTTCTGCTGGCTTTTGGCATCAAAAACAACCTGTTTACAGCAGGTAAGT	1125
1268	ATACATGTACTAGTTGTAATAAAATAAATTAACCTCTCGCCCTGAAGCT	1314
1126	ATACATGTACTGAATGTACTAAAAAATAACCTTCTGTCGCCACAGCT	1172
RESULT 5		
AC120669/c	175748 bp	DNA linear
LOCUS	HTG 23-JUL-2002	
DEFINITION	***, 46 unordered pieces.	*** SEQUENCING IN PROGRESS
ACCESSION	AC120669	
VERSION	AC120669.2	GI:21902861
KEYWORDS	HTG: HTGS_PHASE1	
SOURCE	Rattus norvegicus	
ORGANISM	Rattus norvegicus	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
REFERENCE	1 (bases 1 to 175748)	
AUTHORS	Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbara, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wlarczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G. and Gibbs, R.	
Direct Submission		
Unpublished		
2 (bases 1 to 175748)		
Worley, K.C.		
TITLE		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
AUTHORS		
TITLE		
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AUTH		

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 180903)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.K., Ayale,M., Banks,T., Barbara,J., Benton,J., Blmage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brleva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carton,F.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,K., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,B., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gundaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogue,M., Holloway,C., Hollins,B., Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Martindale,A., Martinez,E., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Meigs,G., Metzker,M., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Morgan,M., Morris,S., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonalike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Woodson,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstein,G. and Gibbs,R.

Direct Submission

Unpublished

2 (bases 1 to 180903)

Worley,K.C.

Direct Submission

Submitted (02-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 180903)

Worley,K.C.

Direct Submission

Submitted (23-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GWUQ

Center clone name: CH230-35H21

----- Summary Statistics

Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 117810 bases at least Q40

Consensus quality: 124839 bases at least Q30

Consensus quality: 130161 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 69 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1
1019 1018: contig of 1018 bp in length
1118: gap of unknown length
2397: contig of 1279 bp in length
2497: gap of unknown length
2998 3536: contig of 1039 bp in length
3536: gap of unknown length
3537 5038: contig of 1402 bp in length
5038: gap of unknown length
5139 5138: gap of unknown length
5139 6416: contig of 1278 bp in length
6417 6516: gap of unknown length
6517 7782: contig of 1266 bp in length
7783 7882: gap of unknown length
7883 9056: contig of 1174 bp in length
9057 9157: gap of unknown length
9157 10223: contig of 1067 bp in length
10224 10323: gap of unknown length
10324 11849: contig of 1526 bp in length
11850 11949: gap of unknown length
11950 13459: contig of 1510 bp in length
13460 13559: gap of unknown length
13560 15061: contig of 1502 bp in length
15062 15161: gap of unknown length
15162 16401: contig of 1240 bp in length
16402 16501: gap of unknown length
16502 17502: contig of 1001 bp in length
17503 17602: gap of unknown length
17603 18831: contig of 1229 bp in length
18832 18931: gap of unknown length
18932 20133: contig of 1202 bp in length
20134 20233: gap of unknown length
20234 21645: contig of 1412 bp in length
21646 21745: gap of unknown length
21746 23608: contig of 1863 bp in length
23609 23708: gap of unknown length
23709 25221: contig of 1513 bp in length
25222 25321: gap of unknown length
25322 26764: contig of 1443 bp in length
26765 26864: gap of unknown length
26865 28249: contig of 1385 bp in length
28250 28349: gap of unknown length
28350 30014: contig of 1665 bp in length
30015 30114: gap of unknown length
30115 32030: contig of 1916 bp in length
32031 32130: gap of unknown length
32131 35243: contig of 3113 bp in length
35244 35343: gap of unknown length
35344 37525: contig of 2182 bp in length
37526 37625: gap of unknown length
37626 39406: contig of 1780 bp in length
39406 39505: gap of unknown length
39506 41254: contig of 1748 bp in length
41254 41353: gap of unknown length
41354 43191: contig of 1838 bp in length
43192 43291: gap of unknown length
43292 44919: contig of 1627 bp in length
44919 45019: gap of unknown length
45019 46791: contig of 1772 bp in length
46791 48791: gap of unknown length
48791 48866: contig of 1876 bp in length
48867 50304: gap of unknown length
50304 50404: contig of 1438 bp in length
50404: gap of unknown length


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* 50405 52389: contig of 1985 bp in length
* 52390 52489: gap of unknown length
* 52490 54030: contig of 1914 bp in length
* 54030 54503: gap of unknown length
* 54503 56678: contig of 2175 bp in length
* 56678 56779: gap of unknown length
* 56779 58508: contig of 1730 bp in length
* 58508 58609: gap of unknown length
* 58609 60843: contig of 2234 bp in length
* 60843 60943: gap of unknown length
* 60943 62623: contig of 1681 bp in length
* 62623 62723: gap of unknown length
* 62723 65156: contig of 2433 bp in length
* 65156 65256: gap of unknown length
* 65256 66557: contig of 1301 bp in length
* 66557 66658: gap of unknown length
* 66658 69117: contig of 2460 bp in length
* 69117 69217: gap of unknown length
* 69217 71292: contig of 2075 bp in length
* 71292 71393: gap of unknown length
* 71393 73471: contig of 2078 bp in length
* 73471 73571: gap of unknown length
* 73571 75334: contig of 1764 bp in length
* 75334 75434: gap of unknown length
* 75434 78268: contig of 2834 bp in length
* 78268 78369: gap of unknown length
* 78369 81339: contig of 2971 bp in length
* 81339 81439: gap of unknown length
* 81439 84539: contig of 3100 bp in length
* 84539 84639: gap of unknown length
* 84639 87363: contig of 2724 bp in length
* 87363 87464: gap of unknown length
* 87464 89602: contig of 2139 bp in length
* 89602 89703: gap of unknown length
* 89703 92192: contig of 2490 bp in length
* 92192 92293: gap of unknown length
* 92293 94766: contig of 2473 bp in length
* 94766 98585: gap of unknown length
* 98585 98684: gap of unknown length
* 98684 100661: contig of 1977 bp in length
* 100661 100761: gap of unknown length
* 100761 103351: contig of 2590 bp in length
* 103351 103452: gap of unknown length
* 103452 105311: contig of 1860 bp in length
* 105311 105411: gap of unknown length

Query Match      6.8%; Score 96; DB 2: Length 180903;
Best Local Similarity 40.1%; Pred. No. 8.5e-08;
Matches 398; Conservative 0; Mismatches 590; Indels 4; Gaps 1;

QY 369 TAATGAAATGCTCCAAATTTTAATGCAGGTGCTAGTACATGCACAGCTTGTCCGGTAAA 428
Db 149053 TATTACTACTGCTGCTACTATTGCTACTGCTGCTACTACTACTACTGCTGCTACTGCT 148994

QY 429 CAGAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148994
Db 148993 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148994

QY 489 CGCATGCTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148994
Db 148933 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148933

QY 549 CAGAGTGTGTAATGTAGCTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148934
Db 148873 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 148874

QY 609 TTTCAATCCAGTAAAGTAAATGACACACCTTGTCCCGCAATTAACCTGCTGCTGCTGCTGCTGCT 148874
Db 148813 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 148813

QY 669 TTAAGCTACTTGTAGTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148754

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Db 148753 TACAACTACTACTACTACTATTATTACTACTACTGCTGCTGCTACTACTACTACTACTACT 148694
QY 729 TGGTACTTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 788
Db 148693 TTATACTACTACTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148634
QY 789 TTGTGCTCCTAACTTTTACAAATAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 848
Db 148633 TACCACCTACTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148574
QY 849 CCTACCTTGGCCCAACAATAAAGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 908
Db 148573 TACTACTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148514
QY 909 TTTAGCCCAATAATG----TAATATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 964
Db 148513 TAACCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148454
QY 965 CAACCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1024
Db 148453 CCACCTACTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148394
QY 1025 ATGCTAATAATTTCTAGCGAGGAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 1084
Db 148393 CTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148334
QY 1085 AAGCGCTGTAGCAACTGCGAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1144
Db 148333 CTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148274
QY 1145 GCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1204
Db 148273 CTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148214
QY 1205 AATGTGTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1264
Db 148213 CTATTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148154
QY 1265 TTGATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1324
Db 148153 CTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148094
QY 1325 AATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1356
Db 148093 CTACTATTACTACTACTATAGAACCTTAGGTTTC 148062

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RESULT 7
AC022322/c
LOCUS
DEFINITION
Homo sapiens chromosome 6 clone RP11-317M22, WORKING DRAFT
SEQUENCE, 16 unordered pieces.
ACCESSION
AC022322
VERSION
AC022322.3 GI:7321964
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 186935)
AUTHORS
Waterston,R.H.
TITLE
The sequence of Homo sapiens clone
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 186935)
AUTHORS
Waterston,R.H.
TITLE
Direct Submission
JOURNAL
Submitted (30-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT
On Mar 24, 2000 this sequence version replaced gi:7109575.
----- Genome Center -----
Center: Washington University Genome Sequencing Center

```

[illegible]

QY 759 TTGGTAGCACAACACTGAATGACTACTAATTTGCTCCCTAACTTTTACAATAATATGC 818
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 QY 819 TCCTAATTTCAATCCAGGTAATAGTACATGCTACCTTTGCCAGCAATAAAGATTATGG 878
 Db 7776 TGTTGCTGTTGCTGCTGCTATTTGCTGTTGTTAAATTTGTCATCTATTTGCTGTTGCTGA 7717
 QY 879 TGCTGAAGCCACTGCAGGTGCTGCTGCTACTTTAGCCAAATAATGTAATATTCGATGCC 938
 Db 7716 TGCTGCTGTTGCTATTTGCTGTTGCTGCTACTGTTGCTATTTGCTGTTGCTTTGTTGCTG 7657
 QY 939 TGATGGTACTGCAATGCTAGTGAGCAACTAATTTAGTAATATATAACAGAACTCT 998
 Db 7656 TCTTTGTTGCTGCTGCTACTGATG---CTGTTGCTGCTATTTATTTGCTGCTGCTGCTGT 7600
 QY 999 AATTTGCTGCTAACCTTTATTTTGTAGTGAATAATTTCTAGCCAGGAATAGTAGATG 1058
 Db 7599 TGCTGTTGTTGCTGCTGCTATTTGCTGTTGTTGCTGTTGCTGCTGCTGCTGCTAT 7540
 QY 1059 CAAGCATGTCAGCAATAAAGTTTAAAGCGCTGTAGCAACTGCAGGTGCTGCTGCTAC 1118
 Db 7539 TGCTGTTGCTGCTACTATTTGCTGTTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTG 7480
 QY 1119 TTTAATTTGCATAATGTCCTTGAATGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1178
 Db 7479 TACTGTTGTTGCTACTATGCTAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTAT 7420
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 Db 7419 TACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7360
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 QY 1299 TTCTGGCGCTGAAGCTAATTTACCTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1336
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RESULT 8
 AC024253
 LOCUS
 DEFINITION Homo sapiens chromosome 6 clone RP11-758C19, WORKING DRAFT
 AC024253
 VERSION AC024253.4 GI:9959959
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 179553)
 Waterston,R.H.
 The sequence of Homo sapiens clone
 Unpublished
 2 (bases 1 to 179553)
 Waterston,R.H.
 Direct Submission
 Submitted (28-FEB-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 On Sep 1, 2000 this sequence version replaced gi:8568958.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc/index.shtml

 Project Information -----
 Center project name: H.NH0758C19

 Summary Statistics -----
 Sequencing vector: M13; 100%

Sequencing vector: plasmid; 0%
 Chemistry: Dye-primer ET; 100% of reads
 Chemistry: Dye-terminator Big Dye; 0% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 175235 bases at least Q40
 Consensus quality: 176522 bases at least Q30
 Consensus quality: 177171 bases at least Q20
 Insert size: 198000; agarose-fp
 Quality coverage: 4.48 in Q20 bases; agarose-fp
 Quality coverage: 4.99 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 12 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
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 * 7554: contig of 7554 bp in length
 * 7555: gap of unknown length
 * 7655: 16349: contig of 8695 bp in length
 * 16350: 16449: gap of unknown length
 * 16450: 26475: contig of 10026 bp in length
 * 26476: 35880: contig of 9305 bp in length
 * 35881: 62010: contig of unknown length
 * 35882: 62010: contig of 26030 bp in length
 * 62011: 90565: contig of 28455 bp in length
 * 90566: 90665: gap of unknown length
 * 90666: 117183: contig of 26518 bp in length
 * 117184: 163019: contig of 45736 bp in length
 * 163020: 163119: gap of unknown length
 * 163120: 166938: contig of 3819 bp in length
 * 166939: 167039: gap of unknown length
 * 167039: 169412: contig of 2274 bp in length
 * 169413: 171639: contig of 2227 bp in length
 * 171640: 171739: gap of unknown length
 * 171740: 179553: contig of 7814 bp in length.
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 /chromosome="6"
 /clone="RP11-758C19"
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 /note="assembly_name:Contig6"
 169413..171639
 /note="assembly_name:Contig7"

Thu Feb 20 11:10:09 2003

us-09-497-967-3.rge

Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
 Usmani,K., Vasquez,L., Vera,V., Villaion,D., Vinson,R., Wang,Q.,
 Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
 Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
 Weinstein,G. and Gibbs,R.
 Direct Submission
 Unpublished
 2 (bases 1 to 176822)
 Worley,K.C.
 Direct Submission
 Submitted (09-NOV-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 176822)
 Worley,K.C.
 Direct Submission
 Submitted (12-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 11, 2002 this sequence version replaced gi:18846108.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GZV
 Center clone name: CH230-9811
 ----- Summary Statistics
 Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 115453 bases at least Q40
 Consensus quality: 125501 bases at least Q30
 Consensus quality: 133023 bases at least Q20

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 77 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 *
 * 1 1052: contig of 1052 bp in length
 * 1053 1152: gap of unknown length
 * 1153 2179: contig of 1027 bp in length
 * 2180 2279: gap of unknown length
 * 2280 3355: contig of 1076 bp in length
 * 3356 3455: gap of unknown length
 * 3456 4834: contig of 1379 bp in length
 * 4835 4934: gap of unknown length
 * 4935 6222: contig of 1288 bp in length
 * 6223 6323: gap of unknown length
 * 6323 7400: contig of 1078 bp in length
 * 7401 7500: gap of unknown length
 * 7501 8807: contig of 1307 bp in length
 * 8808 8907: gap of unknown length
 * 8908 10266: contig of 1359 bp in length
 * 10267 10366: gap of unknown length
 * 10367 11662: contig of 1296 bp in length
 * 11663 12812: gap of unknown length
 * 12812 12913: contig of 1050 bp in length
 * 12913 14136: contig of 1224 bp in length
 * 14137 14237: gap of unknown length
 * 14237 15446: contig of 1210 bp in length
 * 15447 15547: gap of unknown length
 * 15547 16866: contig of 1320 bp in length
 * 16867 16966: gap of unknown length

16967 18700: contig of 1734 bp in length
 18701 18800: gap of unknown length
 18801 20358: contig of 1558 bp in length
 20359 20458: gap of unknown length
 20459 22025: contig of 1567 bp in length
 22026 22125: gap of unknown length
 22126 24515: contig of 2390 bp in length
 24516 25846: contig of 1231 bp in length
 25847 27176: contig of unknown length
 27177 27276: contig of 1230 bp in length
 27277 28283: contig of 1007 bp in length
 28284 28383: gap of unknown length
 28384 29995: contig of 1612 bp in length
 29996 30095: gap of unknown length
 30096 31459: contig of 1364 bp in length
 31460 31559: gap of unknown length
 31560 32924: contig of 1365 bp in length
 32925 34073: contig of 1049 bp in length
 34074 34173: gap of unknown length
 34174 35425: contig of 1252 bp in length
 35426 35980: gap of unknown length
 35981 37080: gap of unknown length
 37081 38628: contig of 1548 bp in length
 38629 38728: gap of unknown length
 38729 40212: contig of 1484 bp in length
 40213 40312: gap of unknown length
 40313 42052: contig of 1740 bp in length
 42053 42152: gap of unknown length
 42153 43337: contig of 1185 bp in length
 43338 43437: gap of unknown length
 43438 45526: contig of 2089 bp in length
 45527 45626: gap of unknown length
 45627 46889: contig of 1263 bp in length
 46890 46989: gap of unknown length
 46990 48670: contig of 1681 bp in length
 48671 48770: gap of unknown length
 48771 50070: contig of 1300 bp in length
 50071 50170: gap of unknown length
 50171 51389: contig of 1219 bp in length
 51390 51489: gap of unknown length
 51490 53145: contig of 1656 bp in length
 53146 53245: gap of unknown length
 53246 54620: contig of 1375 bp in length
 54621 54720: gap of unknown length
 54721 56920: contig of 2200 bp in length
 56921 57021: gap of unknown length
 57021 59065: contig of 2045 bp in length
 59066 59165: gap of unknown length
 59166 60712: contig of 1547 bp in length
 60713 60812: gap of unknown length
 60813 61876: contig of 1064 bp in length
 61877 64778: contig of 2802 bp in length
 64779 64878: gap of unknown length
 64879 66792: contig of 1914 bp in length
 66793 66892: gap of unknown length
 66893 68575: gap of unknown length
 68576 70134: contig of 1459 bp in length
 70135 70234: gap of unknown length
 70235 72222: contig of 1988 bp in length
 72223 72322: gap of unknown length
 72323 73655: contig of 1333 bp in length
 73656 73755: gap of unknown length
 73756 76619: contig of 2864 bp in length
 76620 76719: gap of unknown length
 76720 78861: contig of 2142 bp in length
 78862 78961: gap of unknown length
 78962 81654: contig of 2693 bp in length


```

Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L17592
Center clone name: 107_G_22
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 243729 bases at least Q40
Consensus quality: 251231 bases at least Q30
Consensus quality: 253857 bases at least Q20
Insert size: 220000; agarose-1p
Insert size: 255004; sum-of-contigs
Quality coverage: 8.2 in Q20 bases; agarose-1p
Quality coverage: 7.1 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 67 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
* 1 641: contig of 641 bp in length
*
* 642 741: gap of 100 bp
*
* 742 1156: contig of 415 bp in length
*
* 1157 1256: gap of 100 bp
*
* 1257 1891: contig of 635 bp in length
*
* 1892 1991: gap of 100 bp
*
* 1992 2942: contig of 951 bp in length
*
* 2943 3042: gap of 100 bp
*
* 3043 4004: contig of 962 bp in length
*
* 4005 4104: gap of 100 bp
*
* 4105 4797: contig of 693 bp in length
*
* 4798 4897: gap of 100 bp
*
* 4898 5626: contig of 729 bp in length
*
* 5627 5726: gap of 100 bp
*
* 5727 6421: contig of 695 bp in length
*
* 6422 6521: gap of 100 bp
*
* 6522 7622: contig of 1101 bp in length
*
* 7623 7722: gap of 100 bp
*
* 7723 8353: contig of 631 bp in length
*
* 8354 8453: gap of 100 bp
*
* 8454 9092: contig of 639 bp in length
*
* 9093 9192: gap of 100 bp
*
* 9193 10104: contig of 912 bp in length
*
* 10105 10204: gap of 100 bp
*
* 10205 10848: contig of 644 bp in length
*
* 10849 10948: gap of 100 bp
*
* 10949 11899: contig of 951 bp in length
*
* 11900 11999: gap of 100 bp
*
* 12000 12601: contig of 602 bp in length
*
* 12602 12701: gap of 100 bp
*
* 12702 13401: contig of 700 bp in length
*
* 13402 13501: gap of 100 bp
*
* 13502 13936: contig of 435 bp in length
*
* 13937 14036: gap of 100 bp
*
* 14037 14681: contig of 645 bp in length
*
* 14682 14781: gap of 100 bp
*
* 14782 15812: contig of 1031 bp in length
*
* 15813 15912: gap of 100 bp
*
* 15913 16579: contig of 667 bp in length
*
* 16580 16679: gap of 100 bp
*
* 16680 17502: contig of 823 bp in length
*
* 17503 17602: gap of 100 bp
*
* 17603 18647: contig of 1045 bp in length
*
* 18648 18747: gap of 100 bp
*
* 18748 19879: contig of 1132 bp in length
*
* 19880 19979: gap of 100 bp
*
* 19980 21001: contig of 1022 bp in length
*
* 21002 21101: gap of 100 bp

```

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 57 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1478: contig of 1478 bp in length
* 1479 1578: gap of unknown length
* 1579 2917: contig of 1339 bp in length
* 2918 3017: gap of unknown length
* 3018 4096: contig of 1079 bp in length
* 4097 4196: gap of unknown length
* 4197 5642: contig of 1446 bp in length
* 5643 5742: gap of unknown length
* 5743 6939: contig of 1197 bp in length
* 6940 7040 8481: gap of unknown length
* 8482 10097 10196: gap of unknown length
* 10197 11452: contig of 1256 bp in length
* 11453 11552: gap of unknown length
* 11553 12648: contig of 1096 bp in length
* 12649 12749 14133: contig of 1385 bp in length
* 14134 14233: gap of unknown length
* 14234 15551: contig of 1318 bp in length
* 15552 15651: gap of unknown length
* 15652 17024: contig of 1373 bp in length
* 17025 18147: contig of 1023 bp in length
* 18148 18247: gap of unknown length
* 18248 19923: contig of 1676 bp in length
* 19924 21045: contig of 1022 bp in length
* 21046 21145: gap of unknown length
* 21146 22252: contig of 1147 bp in length
* 22253 22392: gap of unknown length
* 22393 23545: contig of 1153 bp in length
* 23546 23645: gap of unknown length
* 23646 25288: contig of 1643 bp in length
* 25289 25389: gap of unknown length
* 25390 26988: contig of 1600 bp in length
* 26989 27088: gap of unknown length
* 27089 29137 29236: gap of unknown length
* 29237 30361: contig of 1125 bp in length
* 30362 30461: gap of unknown length
* 30462 31728: contig of 1267 bp in length
* 31729 31828: gap of unknown length
* 31829 33326: contig of 1498 bp in length
* 33327 33426: gap of unknown length
* 33427 34972: contig of 1546 bp in length
* 34973 35072: gap of unknown length
* 35073 37098: contig of 2026 bp in length
* 37099 37198: gap of unknown length
* 37199 38876: contig of 1678 bp in length
* 38877 38976: gap of unknown length
* 38977 40520: contig of 1544 bp in length
* 40521 40620: gap of unknown length
* 40621 41712: contig of 1092 bp in length
* 41713 41812: gap of unknown length
* 41813 43711: contig of 1899 bp in length
* 43712 43811: gap of unknown length
* 43812 45722: contig of 1911 bp in length
* 45723 45822: gap of unknown length
* 45823 47646: contig of 1824 bp in length
* 47647 47746: gap of unknown length

* 47747 49427: contig of 1681 bp in length
* 49428 51247: gap of unknown length
* 51248 51347: contig of 1720 bp in length
* 51348 53372: gap of unknown length
* 53373 53473: gap of 2025 bp in length
* 53473 53773: gap of unknown length
* 53773 55965: contig of 2493 bp in length
* 55966 56065: gap of unknown length
* 56066 58604: contig of 2539 bp in length
* 58605 58704: gap of unknown length
* 58705 61433: contig of 2729 bp in length
* 61434 61533: gap of unknown length
* 61534 63097: contig of 1564 bp in length
* 63098 63197: gap of unknown length
* 63198 65272: contig of 2075 bp in length
* 65273 65372: gap of unknown length
* 65373 67765: contig of 2393 bp in length
* 67766 67865: gap of unknown length
* 67866 68952: contig of 1087 bp in length
* 68953 69052: gap of unknown length
* 69053 72102: contig of 3050 bp in length
* 72103 72202: gap of unknown length
* 72203 74585: contig of 2383 bp in length
* 74586 74685: gap of unknown length
* 74686 77412: contig of 2727 bp in length
* 77413 77512: gap of unknown length
* 77513 80330: contig of 2818 bp in length
* 80331 80430: gap of unknown length
* 80431 82126: contig of 1696 bp in length
* 82127 82226: gap of unknown length
* 82227 84702: contig of 2476 bp in length
* 84703 84802: gap of unknown length
* 84803 88989: contig of 4187 bp in length
* 88990 92993: contig of 3904 bp in length
* 92994 93093: gap of unknown length
* 93094 96037: contig of 2944 bp in length
* 96038 96137: gap of unknown length
* 96138 100350: contig of 4213 bp in length
* 100351 100450: gap of unknown length
* 100451 104033: contig of 3583 bp in length
* 104034 104133: gap of unknown length
* 104134 106965: contig of 2832 bp in length
* 106966 107065: gap of unknown length
* 107066 112233: contig of 5168 bp in length

Query Match 6.1%; Score 85.4; DB 2; Length 127354;
Best Local Similarity 45.4%; Pred. No. 6.7e-06;
Matches 308; Conservative 0; Mismatches 371; Indels 0; Gaps 0;

Qy 614 ATCCAGTAAAGTTAATGCACACCTTGTCCGCAATTAACCTGCTAATGTTGCTTAAG 673
Db 118142 AGCAAGACTAAACTGAATGGTTACTACTGCTACTACTACTACTGCTGCTACTACTACAG 118201
Qy 674 CTACTTTAGTGAATGCTACATAACCCGCAATAATGTAACGTTGCATGCCCTGATGGTA 733
Db 118202 CTGCTATTACTACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTAG 118261
Qy 734 CTATAAGTGTGCTGGAGTAAATAATTTGGGTAGCACAACACTGAATGTACTAATTGTG 793
Db 118262 CTACTGCTGCTACTACTACTACTGCTGCTACTACTACTACTACTACTACTACTACTG 118321
Qy 794 CTCCTAATTTTACAATAAATAGTCTCTAATTTCAATCCAGTAAATAGTACATGCTAC 853
Db 118322 CTGCTGCTACTACTACTACTGCTGCTACTACTACTACTACTACTACTACTACTACTAATA 118381
Qy 854 CTGCCCCAGCAATAAAGATTATGGTCTGAAGCCACTGCAGGTGGGCGGCTACTTTAG 913
Db 118382 CTACTGCTGCTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTG 118441
Qy 914 CCAATAATGTAATTTGTCATGCCCTGATGGTACTGCAATTGCTAGTGGAGCAACTAATT 973
Db 118442 CTGCTACTACTACTGTTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTA 118501

* 15989 16088: gap of unknown length
* 16089 17334: contig of 1246 bp in length
* 17335 17434: gap of unknown length
* 17436 18536: contig of 1102 bp in length
* 18537 18636: gap of unknown length
* 18637 20392: contig of 1756 bp in length
* 20393 20492: gap of unknown length
* 20493 21734: contig of 1242 bp in length
* 21735 21834: gap of unknown length
* 21835 23070: contig of 1236 bp in length
* 23071 24215: contig of 1045 bp in length
* 24216 24315: gap of unknown length
* 24316 25375: contig of 1060 bp in length
* 25376 25475: gap of unknown length
* 25476 26523: contig of 1048 bp in length
* 26524 26623: gap of unknown length
* 26624 28311: contig of 1688 bp in length
* 28312 28411: gap of unknown length
* 28412 29686: contig of 1275 bp in length
* 29687 29786: gap of unknown length
* 29787 31163: contig of 1377 bp in length
* 31164 31263: gap of unknown length
* 31264 32573: contig of 1310 bp in length
* 32574 32673: gap of unknown length
* 32674 33936: contig of 1263 bp in length
* 33937 34036: gap of unknown length
* 34037 36010: contig of 1974 bp in length
* 36011 36110: gap of unknown length
* 36111 37486: contig of 1376 bp in length
* 37487 37586: gap of unknown length
* 37587 39435: contig of 1849 bp in length
* 39436 39535: gap of unknown length
* 39536 41146: contig of 1611 bp in length
* 41147 41246: gap of unknown length
* 41247 43121: contig of 1875 bp in length
* 43122 43221: gap of unknown length
* 43222 44577: contig of 1356 bp in length
* 44578 44677: gap of unknown length
* 44678 45896: contig of 1219 bp in length
* 45897 45996: gap of unknown length
* 45997 47598: contig of 1602 bp in length
* 47599 47698: gap of unknown length
* 47699 49203: contig of 1505 bp in length
* 49204 49303: gap of unknown length
* 49304 50831: contig of 1528 bp in length
* 50832 50931: gap of unknown length
* 50932 52280: contig of 1349 bp in length
* 52281 52380: gap of unknown length
* 52381 53520: contig of 1140 bp in length
* 53521 53620: gap of unknown length
* 53621 55537: contig of 1917 bp in length
* 55538 55637: gap of unknown length
* 55638 57202: contig of 1565 bp in length
* 57203 57302: gap of unknown length
* 57303 59447: contig of 2145 bp in length
* 59448 59547: gap of unknown length
* 59548 62351: contig of 2804 bp in length
* 62352 62451: gap of unknown length
* 62452 64457: contig of 2006 bp in length
* 64458 64557: gap of unknown length
* 64558 66031: contig of 1474 bp in length
* 66032 66131: gap of unknown length
* 66132 69637: contig of 3506 bp in length
* 69638 69737: gap of unknown length
* 69739 72323: contig of 2586 bp in length
* 72324 72423: gap of unknown length
* 72424 74742: contig of 2319 bp in length
* 74743 74842: gap of unknown length
* 74843 77069: contig of 2227 bp in length
* 77070 77169: gap of unknown length
* 77170 80560: contig of 3391 bp in length
* 80561 80660: gap of unknown length

* 80661 84125: contig of 3465 bp in length
* 84126 84225: gap of unknown length
* 84226 86431: contig of 2206 bp in length
* 86432 86531: gap of unknown length
* 86532 91371: contig of 4840 bp in length
* 91372 91471: gap of unknown length
* 91472 93957: contig of 2486 bp in length
* 93958 94057: gap of unknown length
* 94058 96162: contig of 2105 bp in length

Query Match 6.1%; Score 85.4; DB 2; Length 155019;
Best Local Similarity 45.4%; Pred. No. 6.4e-06;
Matches 308; Conservative 0; Mismatches 371; Indels 0; Gaps 0;

QY 614 ATCCAGTAAAGTTAATGCACACCTTGTCCGGCAATTAACCTGCTAATGTGCTTAAG 673
Db 109880 AGCAAGACTAACTGAATGGTACTACTGCTACTACTACTGCTGCTACTACTACAG 109939

QY 674 CTACTTTAGGTAAATGCTACAATAACCGGCAATGTAACGTTGCATGCCCTGATGTA 733
Db 109940 CTGCTATTACTACTGCTACTACTACTGCTACTACTACTACTACTACTACTACT 109999

QY 734 CTATACTGCTGCTGGAGTAATAATTGGTAGCACAAAACACTGAATGCTACTAATTGT 793
Db 110000 CTACTGCTGCTACTACTACTGCTGCTGCTACTACTACTACTACTACTACTACT 110059

QY 794 CTCCTAACTTTTACAATAATAATGCTCCCTAATTTCAATCCAGGTAATAGTACATGCCTAC 853
Db 110060 CTGCTGCTACTACTACTGCTGCTACTACTACTGCTGCTGCTACTACTACTACT 110119

QY 854 CTTGCCAGCAATAAAGATTATGGTGTGAAGCCACTGCAGTGGTCCGCTACTTTAG 913
Db 110120 CTACTGCTGCTACTACTACTGCTGCTGCTACTACTACTACTACTACTACTACT 110179

QY 914 CCAATAATGTAATATTGTCATGCCCTGATGGTACTGCAATTCGTAGTGAGCAACTAATT 973
Db 110180 CTGCTACTACTACTGCTGCTACTACTACTACTACTACTACTACTACTACTACT 110239

QY 974 ATGTAATATTAAACAGAAATGCTAAATGCTGCTGCTACTACTACTACTACTACTACT 1033
Db 110240 CTACTGCTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 110299

QY 1034 ATTTCTAGGAGGAGTAGTAGATGCAAAAGCATGTCCAGCAATAAAGTTTAAAGCGCTG 1093
Db 110300 CTACTACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 110359

QY 1094 TAGCAACTGCAGTGGTACTGCTACTTTAATTCATTAATGTCCTGCTGCTGCTGCTG 1153
Db 110360 CTGCTACTGCTGCTACTACTGCTGCTACTACTACTACTACTACTACTACTACT 110419

QY 1154 GTACTGTACTCACCGATGGGAACACATCTATTATAAATAAGCAGCATCTGAATGTGTTA 1213
Db 110420 CTACTACTACTGCTGCTGCTACTACTACTACTACTACTACTACTACTACTACT 110479

QY 1214 AATGTGTCGCAACTTTTATATACAAAATAAACTGATGGGTAGCAGGTATGTATACAT 1273
Db 110480 CTGCTGCTGCTACTACTACTGCTGCTACTACTACTGCTGCTGCTACTACTACT 110539

QY 1274 GTACTAGTTGTAATAAANA 1292
Db 110540 CTACTACTACTAATAATAA 110558

RESULT 14
AY016024

LOCUS AY016024 35793 bp DNA linear VRT 01-FEB-2002
DEFINITION Takifugu rubripes alpha globin gene cluster, complete sequence.
ACCESSION AY016024
VERSION AY016024.1 GI:18463974
KEYWORDS Takifugu rubripes.
SOURCE Takifugu rubripes
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

* 37567 37666: gap of unknown length
* 37667 84472: contig of 46806 bp in length.

FEATURES	Location/Qualifiers
source	1. .84472

```

1. 84472
source
/organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone="241N7"

```

```
/clone_lib="Incyte Genomics"
```

```
misc_feature 1. .10947 /note="assembly_fragment"
```

clone_end:T7

```
vector_side:left"
```

```
misc_feature
11048. .3/366
/note="assembly fragment"
```

```
clone end:sp6
/note-assembly-fragment
```

```
misc feature
vector_side:right
37667.84472
```

Query Match 5.88; Score 81; DB 2; Length 84472;

Best Local Similarity 42.48; Pred. No. 4.3e-05;

Best local similarity (100%) 100%
Matches 441: Conservative 0: Mismatches 600: Indels 0: Gaps 0:

QY 183 TGGTGCTAGTACGTGTACACCTTGTCCTATAAAAAAAGATGCTGGTGCTTAACCAATCC 242

QY 243 ACCTGCTACTGCTAATTTAGTCACATAATGTAACGTTAAATGCCCTGCTGGTACCGCAAT 302

[illegible]

362

2 4 6 8 10 12 14 16 18 20 22 24 26 28 30 32 34 36 38 40 42 44 46 48 50 52 54 56 58 60 62 64 66 68 70 72 74 76 78 80 82 84 86 88 90 92 94 96 98 100

[illegible]

QY 363 TTTTATGAATAATGCTCCAAATTTAAATGCAGGAGCTAGTACATGCACACCTTGTCC 422

[illegible]

423 GGTAAACAGAGTTGGTGGTGCAATTGACTGCTGGTAATGCCGCTACCATAGTCGCATAATG 482

QY 483 TAACGTCGCATGTCCTACTGGTACTGCACCTTGATGATGGAGTAACTACTGATTATGTTAG 542

Db **4772** T G C T G T T G T T G C T G T T G T T G C T G C T G C T A C T G T T G T 4831

2025 RELEASE UNDER E.O. 14176

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QY 603 TACTCCCTTCAATCCAGGTAAAGTAAATGCACACCTTGTCCGGCAATTAACCTTCTAA 604

4892 TGTGCTGCTGCTGTTGTTGCTGCTGTTGTTGCTGCTGCTG 4951

663 TGTTCGTTAAGCTACTTTAGGTAATGATGCTACAATAACCGCATAATGTACGTTGCATG 722

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